

=====

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Oct 04 11:34:29 EDT 2007

=====

\*\*\*\*\*

Reviewer Comments:

<210> 17

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Motif 3 (coiled coil) CORE SEQUENCE

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Xaa can be a stretch of 1 to 6 amino acids

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Xaa can be any amino acid

<220>

<221> MISC\_FEATURE

<222> (8)..(10)

<223> Xaa can be any amino acid

<220>

<221> MISC\_FEATURE

<222> (12)..(13)

<223> Xaa can be any amino acid

<400> 17

Glu	Xaa	Glu	Xaa	Xaa	Arg	Leu	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Leu	Arg
1					5					10				15

The above <223> description of Xaa at location 2 is invalid: "Xaa" can only represent a single amino acid, not a stretch of amino acids. Also, which amino acid(s) does Xaa represent? Please insert 6 Xaa's, adjust the <222> response, and explain which amino acid(s) the Xaa's represent and that some may be missing. Same error in Sequence 18.

\*\*\*\*\*

Application No: 10580085 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2007-09-20 09:17:27.983  
**Finished:** 2007-09-20 09:17:29.893  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 910 ms  
**Total Warnings:** 9  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> CropDesign N.V.  
<120> Seedy1 sequence for making plants having changed growth characteristics

<130> CD-105-PCT

<140> 10580085  
<141> 2007-09-20

<150> US 60/528,113  
<151> 2003-12-09

<150> EP 03104280.7  
<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1  
<211> 1428  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> misc\_feature  
<223> seedy1 coding sequence (CDS0689)

<400> 1  
atgagtgtgt tacaataccc agaagggatt gacccagcag atgttcagat atggaacaat 60  
gcagcatttgcataatggaga ttctgaagat ttgtcttcgc tgaaacgttc ttggctcct 120  
ctgaaacccc ttccgttag gccatcagat tccttgaat ctgatttgc aagtaaggaa 180  
aatcaaactc ctttatttga gaattcatct gttaatctct catctccgtt acccataaag 240  
ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccattcc 300  
aaacagagtc ttgatgagat ggcggctaga aagagccgaa agggaaatga ttccgtgat 360  
gagaagaaaa tagacgagga aattgaagaa attcagatgg agatttagtag gttgagttca 420  
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag 480  
cgaggaaggg ttgtggcagc aaagtttatg gagccaaac aaagtgttat taagattgaa 540  
gagcgtataat caatgagtgc aagaacaaag gtggagcaga gaaggggtct tagtttagga 600  
ccatctgaga ttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt 660  
ctagcaggga caacaaaggc acggcaatttggaaagcaag agatgattat tactcctatt 720

cagccaatac aaaacaggcg aaagtctgt ttttggaaac ttcaagagat tgaagaagag 780  
ggaaaaagg ttcaaggcttag tcctaaatca agaaaaactg ctgcaagaac aatggttaca 840  
acaaggcagg cagttactac aattgcatca aagaagaatt taaaaaaaaga tgatggactt 900  
ttgagttcag ttccagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaat 960  
aagaagcccc agaggccggg gagggttgg gctagtaggt ataatcagag tacaattcag 1020  
tcatcagtag tgagaaagag gtcttacct gaaaatgata aggtgagag taagagaaat 1080  
gataagaaac ggtcggttac tggggaaa acgcgtgtgt ctcactga gagcaagaat 1140  
ttgggtactg aaagtagggt gaaaaagaga tggaaattc ctgtgagat tgtagttcat 1200  
ggaaacacac agagtggaaa atctccacta agcattattt tgaaggctga tttgcttccg 1260  
cgaatttagga ttgctcggtg tgtgaatgag actcttaggg attctggacc tgctaaaaga 1320  
atgatagagt tgataggcaa gaaatcgaa ttctagtg atgaagataa ggagccacct 1380  
gtctgtcaag ttttaagttt tgcagaggaa gatgctgaag aggaataa 1428

<210> 2  
<211> 475  
<212> PRT  
<213> Nicotiana tabacum

<220>  
<221> MISC\_FEATURE  
<223> seedy1 protein (CDS0689)

<400> 2

Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln  
1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser  
20 25 30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro  
35 40 45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro  
50 55 60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys  
65 70 75 80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn  
85 90 95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser  
100 105 110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile  
115 120 125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala  
130 135 140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys  
145 150 155 160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val  
165 170 175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu  
180 185 190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr  
195 200 205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr  
210 215 220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile  
225 230 235 240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu  
245 250 255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys  
260 265 270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile  
275 280 285

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val  
290 295 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn

305

310

315

320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln  
325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn  
340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val  
355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu  
370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His  
385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro  
405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu  
420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys  
435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val  
450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu  
465 470 475

<210> 3

<211> 1336

<212> DNA

<213> Oryza sativa

<220>

<221> misc\_feature

<223> seedyl coding sequence

<400> 3

atggaggagg acccgctcat cccgctggtc cacgtctgga acaacgcccgc cttcgacgac 60

tcctcgtgtt ccagatcgcc ttggctcccc caaagccccg ccgtcgccgc cgtccgcaag 120

ggcgacaagg	agaatcaccg	ccccgagggtt	gttgatgtcg	ccgcggcta	cgacgtcgag	180
gccgagatcg	gccacatcga	ggcggagatc	ctgcgcctct	cgtccggct	ccaccatctc	240
cgcgtctcca	agcagccgga	gcccaaccgc	gacgacgctc	cgatggggga	gatggtcgct	300
aaggtgaggc	cccgcccgag	gggcctcagc	ctcgcccc	tggatgtgat	ctccatcgct	360
aatcgtgaga	agcatccgct	gogcaccaag	cagcctccgg	cgacgcgggg	cagggggctc	420
agcctcgggc	ccatggagat	cgccgcggcg	aaccctaggg	tgcccgccgc	ggcgcaagcat	480
cagcaacagc	aacgcgctgg	cacggcgcgg	atcctgaagc	caatcaagga	gcctccggtg	540
cagcgtcgca	ggggcgtag	cctcgcccg	ttggagatcc	accacggcgt	cggcagcaag	600
gcaccagcgg	cggcgcgagc	caagccgttc	accaccaagc	tcaacgccc	tcgagaagaa	660
acccgaccct	ccaagcaatt	cgcgtcccc	gccaagccat	ggccgtcgag	caatacaagg	720
cagacactgg	actcgaggca	aggaacagca	gcaagtcgag	cgaaggcgag	gagcccgagc	780
cccaggccca	ggaggcaatc	caatggcaag	gctactgaca	caaggggagg	caacaaggtg	840
gtggatgagc	tcaagccaa	aggtgcgtcg	tcaagtca	gccccagcgc	cggccggcc	900
gccactgcca	agaggatggc	ggggagctcc	aagatgaggg	tcatcccag	ccgctacagc	960
ctcactctg	gcgcgtccct	tggaagcagt	ggagcacagg	agaggcgacg	caagcagtct	1020
ctcccaggat	catcagggga	tgcgaaccag	aatgaggaaa	tcaagcgaa	ggtcatcgag	1080
ctttccaatg	atccactctc	tcctcaaacc	atctccaagg	ttgtgtaaat	gtctccaaag	1140
atcaggacca	tgccgcctcc	tgacgagagc	cctcgcgatt	ccggatgcgc	caagcgggtt	1200
gccgaattgg	tcggaaagcg	ctcggttttc	acggctgcag	ccgaggacgg	gcggggcgctc	1260
gacgtcgaaag	cacccgaggc	ggtcgagaa	gcttgagatg	aaccaccatg	gtttgatccg	1320
ttccttccat	cagctc					1336

<210> 4  
 <211> 431  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> MISC\_FEATURE  
 <223> seedy1 protein  
 <400> 4

Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala

1 5 10 15

Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser  
20 25 30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro  
35 40 45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly  
50 55 60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu  
65 70 75 80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly  
85 90 95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly  
100 105 110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg  
115 120 125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro  
130 135 140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His  
145 150 155 160

Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys  
165 170 175

Glu Pro Pro Val Gln Arg Arg Gly Val Ser Leu Gly Pro Leu Glu  
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys  
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser  
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg  
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala

245

250

255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr

260

265

270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly

275

280

285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys

290

295

300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser

305

310

315

320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg

325

330

335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu

340

345

350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro

355

360

365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met

370

375

380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val

385

390

395

400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp

405

410

415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala

420

425

430

<210> 5

<211> 1860

<212> DNA

<213> *Medicago trunculata*

<220>

<221> misc\_feature  
<223> seedyl coding sequence

<400> 5  
aaaaacgtta aggactaaaa atataataaa atttaagtag ggattcataa tggaagcacc 60  
cctatttaca gggatcttaa atataattaa ccctaataatt tatgacagaa accctttga 120  
aatcacatcg gagcgtgtat gagtagccgt ttcacatcca acggccagta agagcgtaac 180  
tttatttctt ccctcttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt 240  
ccctcttca acctcactct tcatttcttc aacccaaacc caaaaaacta atcagattct 300  
tcttaaatct tgaaaccttt ctcccaaaag cacttaaata aaaaagcact taaccatgaa 360  
taacacaaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc 420  
agcattcgat ggtgaagatt tcgccatgaa ttcattttctt gattccatca aagagaatct 480  
aaacccatcc gcatcaaca ttgttccttc ttcaaacaaa agaactattt atgatgaaat 540  
tgcgaaatt gaaagtgaaa ttaagcgatt aacttcgaag ctggaattgc ttctgtgtga 600  
aaaagctgaa agaaaaatcg ctctgaaaa gcgtgttagt ggaattggta ctggaagaat 660  
agttagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acgggtcg 720  
tttcaaggag gagacaccga aacgaaacgg tgtcgttcg gatacgccga aatctagggt 780  
taattggaga agaggatga gtttaggtcc gatggagatt gccggaaag tgatggcacc 840  
gccggcgatg acgattactc cggcgacggt gaatcgagg aagtcttgc ttctggaaacc 900  
gcaggaaagt tgtgaagtaa tgccgtcggt gattactccg gcgacgggtga ataggaggaa 960  
atcttgtttt ttgaaacctc aagaaagtgg tgaagaaaat cgaagaaaaa cgatttgcaa 1020  
accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt 1080  
gaagaagaaa gatgaagaaa ttgctcaggc tcaaccgaag aagctgtttg aaggtgaaaa 1140  
atcagtgaag aaatcggtga aacaaggtag aattgttgca agccggata attccgggtgg 1200  
tggtggtggt gatgcgagga aaagatcggtt ttcggagaat aataagggtt tagggagtga 1260  
aatcagggtct aagaagagat gggagatacc aattgaagaa gtggatgtga gtgggtttgt 1320  
tatgttaccg aagattcga caatgagggtt tggatgtgag agtccctagag attctgggtgc 1380  
tgttaaaaga gttgctgaat tgaatggaaa aagatcttac ttttgcgtatg aagatgagga 1440  
ggagagagtg atggggagg aagaagggtgg ttctgtttgt caggtttga atttgctga 1500  
agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaaat tggaattgtat 1560  
ttgtttttgtt ggggttgggtt ggaactggct atgttctgtc tgattctttt gcattttgggt 1620

gtgaaactaa agatgaggtg aaaagtttat gcttgttaaa ttggattggt ttatatgttt 1680  
tgaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgttt 1740  
ataatgatat ggattaatt tgtatacaca atataatata gtatgcattg agagagttt 1800  
tcgttcagta ttcattctga ttttagtgtt tatctcattc tagaagattg tattttgtg 1860

<210> 6  
<211> 394  
<212> PRT  
<213> *Medicago trunculata*

<220>  
<221> MISC\_FEATURE  
<223> seedyl protein

<400> 6

Met Asn Asn Thr Asn Asn Asn Ile Leu Leu His Ser Thr Gln Val  
1 5 10 15

Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn  
20 25 30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn  
35 40 45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu  
50 55 60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg  
65 70 75 80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly  
85 90 95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys  
100 105 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro  
115 120 125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp  
130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met  
145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys  
165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly  
180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro  
195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn  
210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys  
225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys  
245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg  
260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Asp Ala Arg  
275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg  
290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly  
305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser  
325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys  
340 345